

II. SUMMARY

The foregoing is submitted in response to the "Notice of Non-Compliant Amendment" dated August 15, 2004. In consideration of the preceding amendments and remarks, Applicant hereby respectfully requests reconsideration of all pending claims.

III. INTERVIEW

If the Examiner believes that a telephonic or personal interview would advance the prosecution of the subject application, the Examiner is invited to contact attorney Gildea during business hours at the telephone or facsimile numbers listed below.

IV. FEES

It is believed that no fees are due for consideration of this submission.

V. CORRESPONDENCE/CUSTOMER NUMBER

Please send all correspondence pertaining to this document to:

Applied Biosystems
Attn: Brian D. Gildea, Esq.
15 DeAngelo Drive
Bedford, MA 01730
Telephone: 781-280-2824
Fax: 781-280-2940

IF NOT ALREADY DONE, PLEASE MATCH THIS CASE WITH CUSTOMER NUMBER

23544

Sep 12, 2004
Date

Respectfully submitted
on behalf of Applicant,

Brian D. Gildea
Brian D. Gildea, Esq.
Reg. No. 39,995

Appendix A

III. AMENDMENT

PLEASE ENTER THE FOLLOWING AMENDMENT WITHOUT PREJUDICE OR DISCLAIMER. Applicant reserves the right to file a divisional or continuation application to the originally filed claims.

1. (Currently Amended) A PNA probe of 10 to 30 subunits in length comprising a probing nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-

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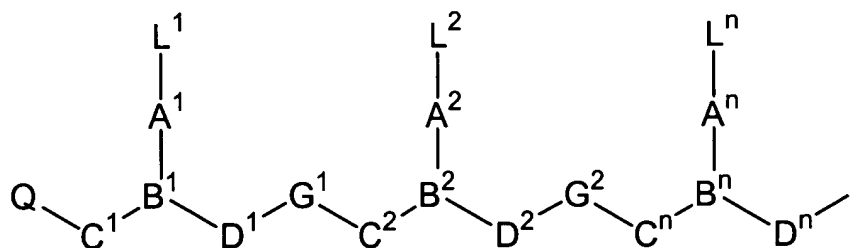
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 ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-
 TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No.
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wherein,

n is at least 2,

each of L¹-Lⁿ is independently selected from the group consisting of hydrogen, hydroxy, (C₁-C₄)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C¹-Cⁿ is (CR⁶R⁷)_y, where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z where R⁶ and R⁷ are as defined above;

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each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2

but not more than 10;

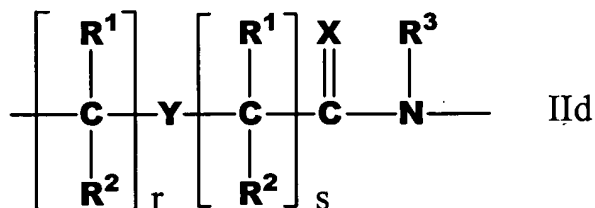
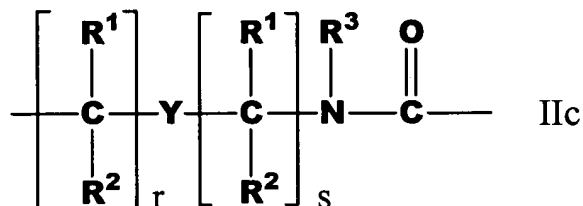
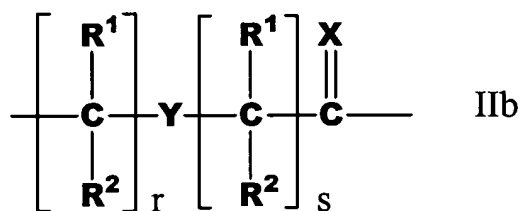
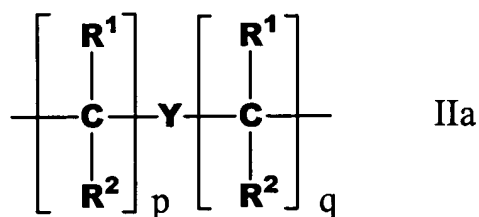
each of G^1-G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation,

where R^3 is as defined above;

each of A^1-A^n and B^1-B^n are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R^3N^+ ; or

(b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se, NR^3 , CH_2 or $C(CH_3)_2$;

Y is a single bond, O, S or NR^4 ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

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each of r and s is zero or an integer from 1 to 5, the sum of $r+s$ being not more than 10;

each R^1 and R^2 is independently selected from the group consisting of hydrogen, (C_1-C_4) alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R^3 and R^4 is independently selected from the group consisting of hydrogen, (C_1-C_4) alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C_1-C_4) alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is $-CO_2H$, $-CONR'R''$, $-SO_3H$ or $-SO_2NR'R''$ or an activated derivative of $-CO_2H$ or $-SO_3H$; and

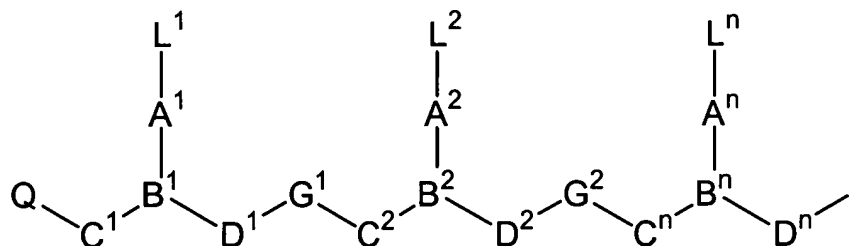
I is $-NHR'''R''''$ or $-NR'''C(O)R''''$, where R' , R'' , R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

(Claims 2-3, Canceled)

4. (Original) The probe of claim 1, wherein the probe is unlabeled.
5. (Original) The probe of claim 1, wherein the probe is labeled with at least one detectable moiety.
6. (Original) The probe of claim 5, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.
7. (Original) The probe of claim 1, wherein the probe is labeled with at least two independently detectable moieties.
8. (Original) The probe of claim 7, wherein the two or more independently detectable moieties are independently detectable fluorophores.

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9. (Original) The probe of claim 1, wherein the probe is support bound.
10. (Currently Amended) A probe set comprising at least thirteen PNA probes of 10 to 30 subunits in length ~~and that is suitable for detecting, identifying or enumerating human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and/or 20, as well as 13/21 as a pair, in a sample wherein said PNA probes have the formula:~~



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$, where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;

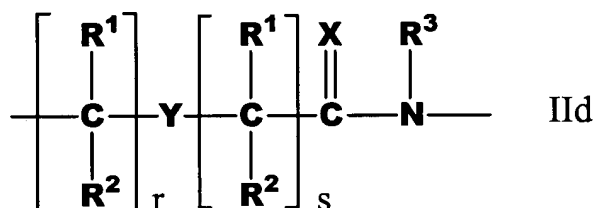
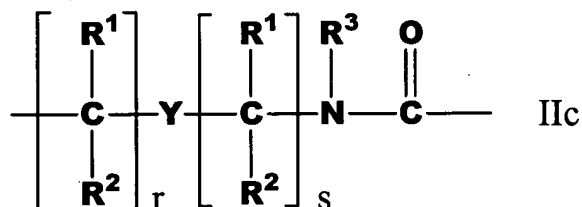
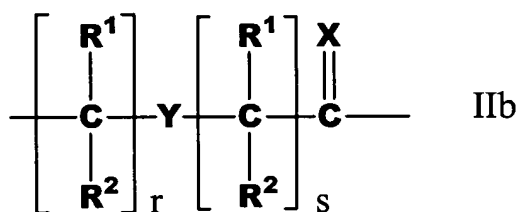
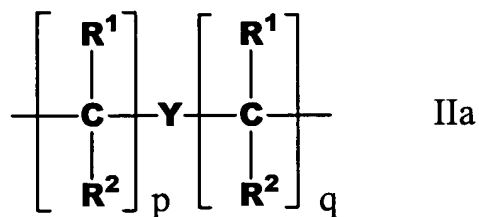
each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

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(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R³N⁺; or

(b) A is a group of formula (IId) and B is CH;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

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each R^3 and R^4 is independently selected from the group consisting of hydrogen, (C_1-C_4) alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C_1-C_4) alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is $-CO_2H$, $-CONR'R''$, $-SO_3H$ or $-SO_2NR'R''$ or an activated derivative of $-CO_2H$ or $-SO_3H$; and

I is $-NHR'''R''''$ or $-NR'''C(O)R''''$, where R' , R'' , R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:
the one or more PNA probes of the set specific for detecting human chromosome X comprise a probing nucleobase sequence selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome Y comprise a probing nucleobase sequence selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16), or the complement to any of the foregoing sequences;

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the one or more PNA probes of the set specific for detecting human chromosome 1 comprise a probing nucleobase sequence, selected from the group consisting of:

AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17) and CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 2 comprise a probing nucleobase sequence selected from the group consisting of:

GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25) and TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 3 comprise a probing nucleobase sequence selected from the group consisting of:

ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-

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AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 4 comprise a probing nucleobase sequence selected from the group consisting of:

ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 6 comprise a probing nucleobase sequence selected from the group consisting of:

CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq.

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ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63) and TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 7 comprise a probing nucleobase sequence selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 8 comprise a probing nucleobase sequence selected from the group consisting of:

ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 9 comprise a probing nucleobase sequence selected from the group consisting of:

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ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 10 comprise a probing nucleobase sequence selected from the group consisting of:

AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76) and GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 11 comprise a probing nucleobase sequence selected from the group consisting of:

AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 12 comprise a probing nucleobase sequence, selected from the group consisting of:

TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No.

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92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96) , or the complement of any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 16 comprise a probing nucleobase sequence selected from the group consisting of:

GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100) and AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 17 comprise a probing nucleobase sequence selected from the group consisting of:

ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110) and AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 18 comprise a probing nucleobase sequence selected from the group consisting of:

TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116);

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GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118) or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 20 comprise a probing nucleobase sequence selected from the group consisting of:

ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152) or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 13/21 comprise a probing nucleobase sequence selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences.

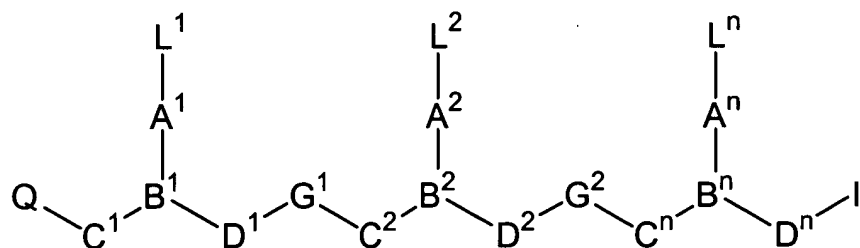
(Claims 11-12; Canceled)

13. (Currently Amended) The probe set of claim ~~11~~ 10, wherein two or more probes of the set are independently detectable.
14. (Original) The probe set of claim 13, wherein one or more of the independently detectable probes are labeled with two or more independently detectable moieties.

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15. (Original) The probe set of claims 13, wherein the independently detectable probes are used to distinguish between human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and 20, as well as 13/21 as a pair.
16. (Previously Amended; Withdrawn) A probe set comprising PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 4 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128) and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$, where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6

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and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1-D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

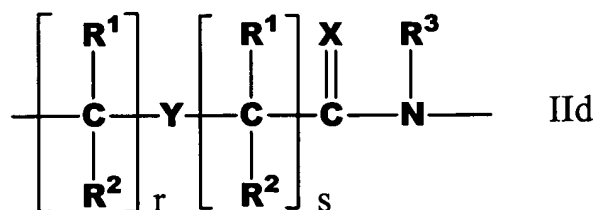
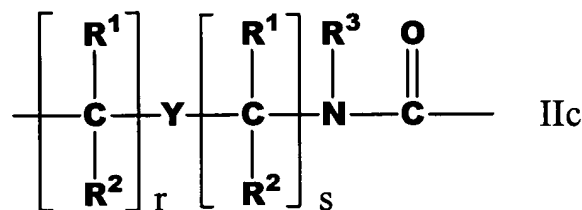
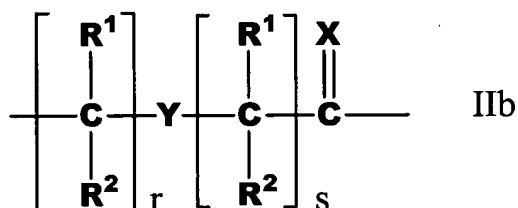
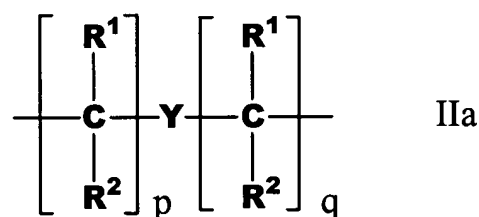
each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;

each of G^1-G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1-A^n and B^1-B^n are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (II d), and B is N or R^3N^+ ; or

(b) A is a group of formula (II d) and B is CH ;



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where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

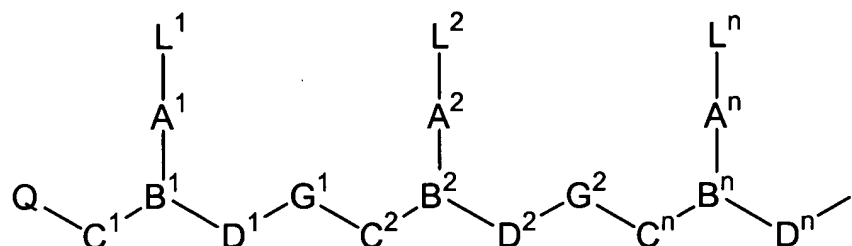
I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

17. (Previously Amended; Withdrawn) A probe set comprising PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 7 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT

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(Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

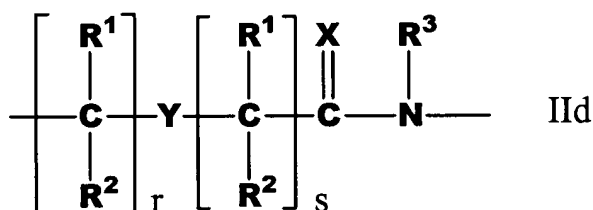
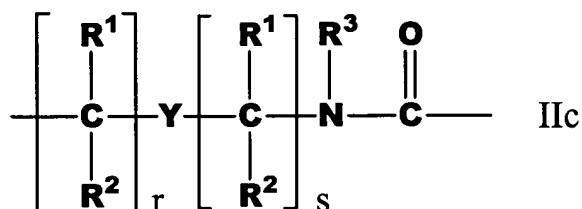
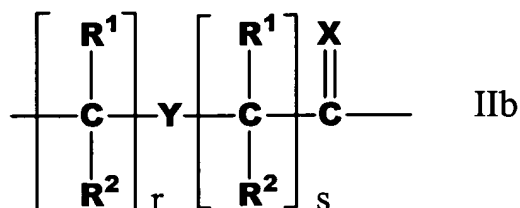
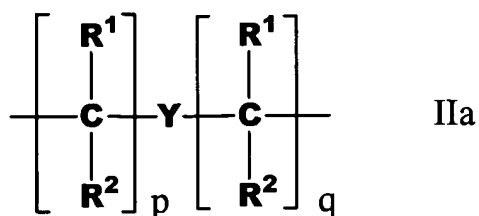
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IId) and B is CH ;

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where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

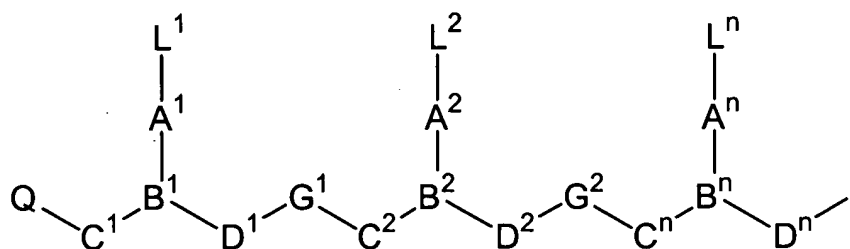
each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

I is $-\text{NHR}'''\text{R}''''$ or $-\text{NR}'''\text{C}(\text{O})\text{R}''''$, where R' , R'' , R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

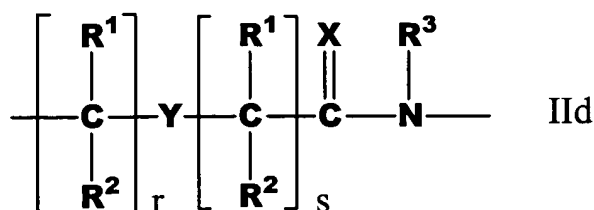
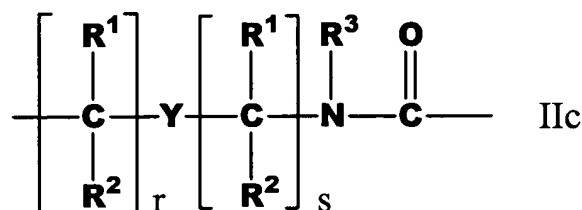
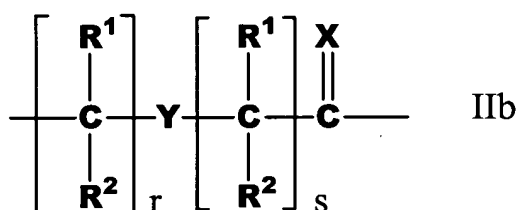
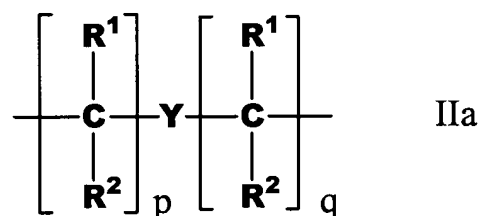
- ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146) wherein said PNA probes have the formula:



each of C¹-Cⁿ is (CR⁶R⁷)_y, where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-

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- C_6)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;
- each of D^1-D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;
- each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;
- each of G^1-G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;
- each of A^1-A^n and B^1-B^n are selected such that:
- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se, NR^3 , CH_2 or $C(CH_3)_2$;

Y is a single bond, O, S or NR^4 ;

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each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

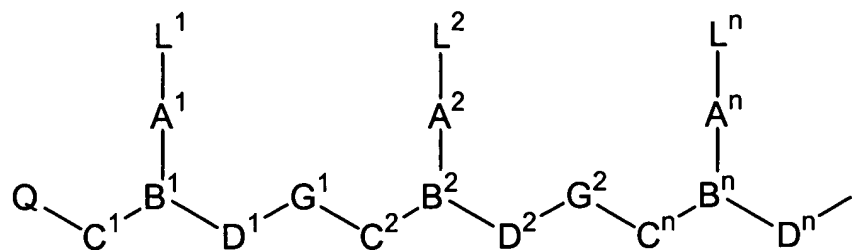
Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

19. (Previously Amended; Withdrawn) A probe set comprising probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 20 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152) wherein said PNA probes have the formula:

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wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

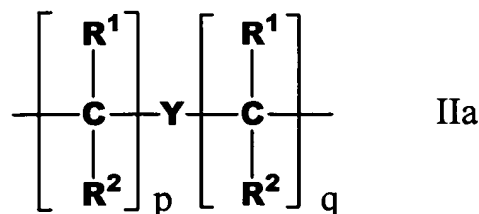
each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;

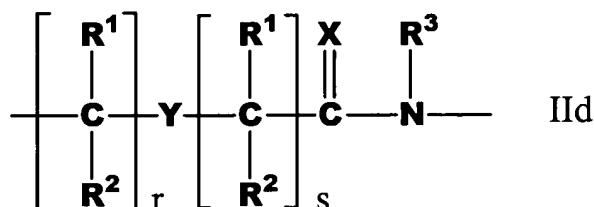
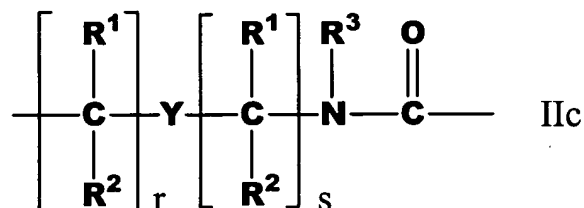
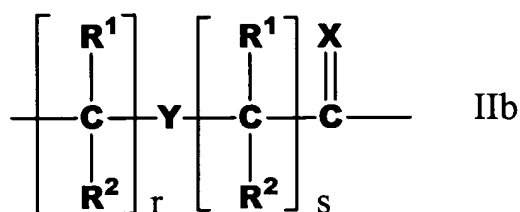
each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IId) and B is CH;



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where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

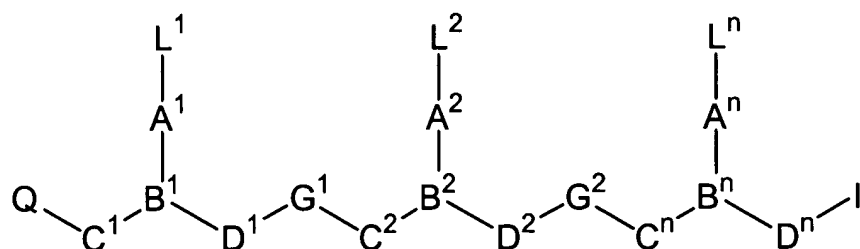
I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,

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amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

20. (Previously Amended; Withdrawn) A probe set comprising PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosomes 13 and 21 as a pair in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159) wherein said PNA probes have the formula:



wherein,

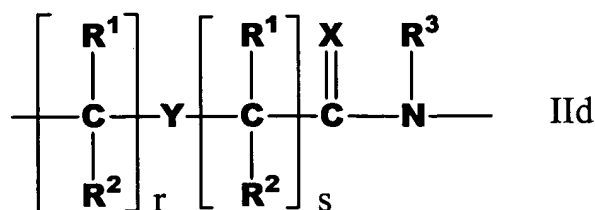
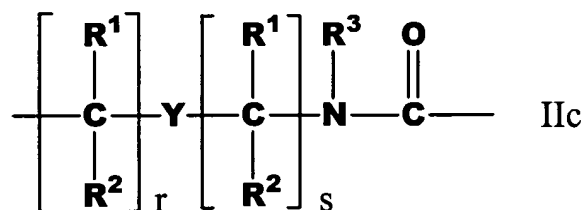
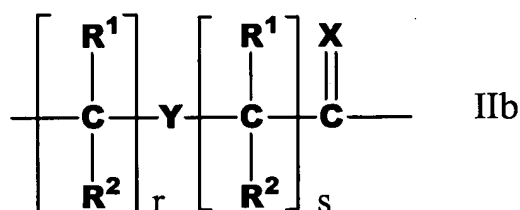
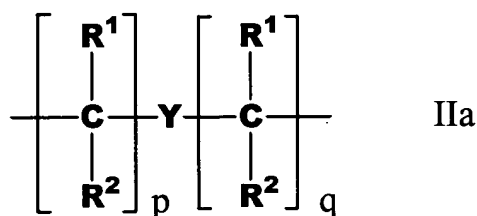
n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$, where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, $(C_1-$

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- C_6 alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1 - C_6)alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;
- each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;
- each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;
- each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;
- each of A^1 - A^n and B^1 - B^n are selected such that:
- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R^3N^+ ; or
 - (b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se, NR^3 , CH_2 or $C(CH_3)_2$;

Y is a single bond, O, S or NR^4 ;

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each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

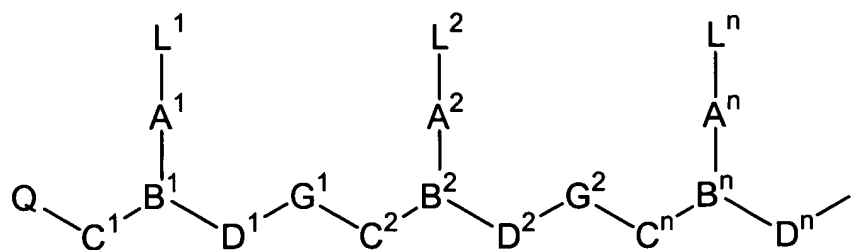
each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

21. (Currently Amended) A method for detecting, identifying or quantitating one or more of human chromosomes Y, 1, 2, 3, 4, 7, 6, 9, 8, 10, 11, 12, 16, 17, 18 or 20, as well as chromosomes 13 and 21 as a pair, in a sample, said method comprising:
- a) contacting the sample with one or more PNA probes of 10 to 30 subunits in length comprising a probing nucleobase sequence which is specific for one or more of human chromosomes Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 or 20, as well as 13/21 as a pair; and
 - b) detecting, identify or quantitating hybridization of the probing nucleobase sequence of the PNA probe or probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes in the sample; wherein said PNA ~~probe or~~ probes have the formula:

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wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

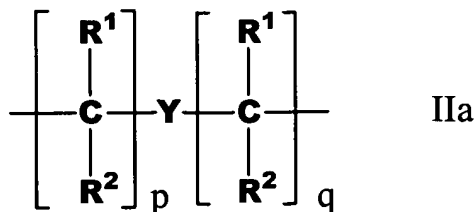
each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;

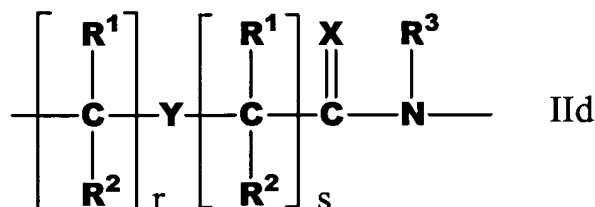
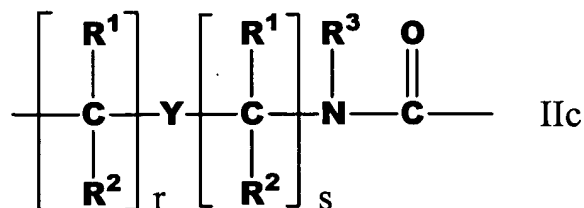
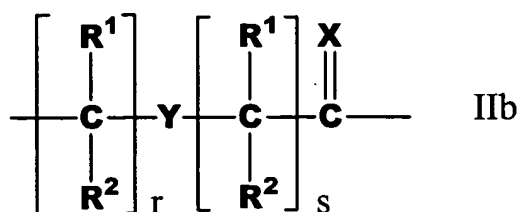
each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IId) and B is CH;



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where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,

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amino protecting groups, reporter ligands, intercalators, chelators,
peptides, proteins, carbohydrates, lipids and steroids and wherein:

the probing nucleobase sequence of the at least one probe comprises
probing nucleobase sequence selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-
AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-
CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID
No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-
AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG
(Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-
TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-
TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20);
GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-
ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID
No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-
GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC
(Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-
GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-
TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No.
30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-
CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No.
33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-
GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq.
ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-
AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG
(Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40);
CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-
AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No.
43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-
GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No.
46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-
CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID

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No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69);

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CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-

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AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159) or the complement to any of the foregoing sequence.

Claims 22-23 (Canceled)

24. (Previously Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 4 is determined by:

- a) contacting the sample with one or more PNA probes of 10 to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-
ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG
(Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122);
TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-
AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID
No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-
TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-

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CCT (Seq. ID No. 128) and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human X chromosomes in the sample.

25. (Previously Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 7 is determined by:

- a) contacting the sample with one or more PNA probes of 10 to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); and

- b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human Y chromosomes in the sample.

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26. (Previously Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 9 is determined by:
- a) contacting the sample with one or more PNA probes of 10 to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:
ATG-ATG-AAA-AAG-GTA-ATA (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146); and
 - b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 1 in the sample.
27. (Previously Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosome 20 is determined by:
- a) contacting the sample with one or more PNA probes of 10 to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:
ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); and
 - b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 2 in the sample.

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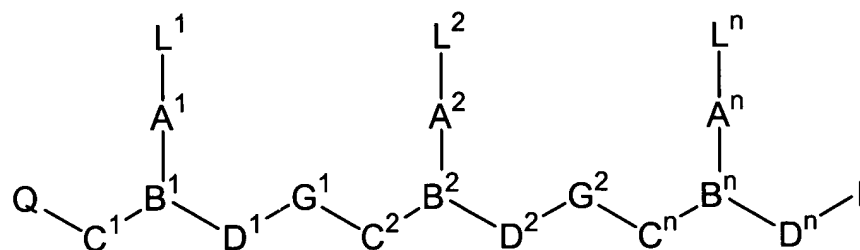
28. (Previously Amended; Withdrawn) The method of claim 23, wherein the presence, absence or number of human chromosomes 13 and 21 as a pair is determined by:
- a) contacting the sample with one or more PNA probes of 10 to 30 subunits in length, wherein at least one probe comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:
 CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159); and
 - b) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 3 in the sample.
29. (Currently Amended) The method of claim ~~23~~ 21, wherein *in-situ* hybridization is used to detect, identify or enumerate human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and 20, as well as 13/21 as a pair, in the sample.
30. (Currently Amended) The method of claim ~~23~~ 21, wherein the method is used to detect or identify chromosome related abnormalities.
31. (Currently Amended) The method of claim ~~23~~ 21, wherein the method is used to detect abnormalities in cells, tissues (including bone marrow), spermatozoa, ova, blastomeres, oocysts, buccal cells and chorionic villi.
32. (Original) The method of claim 31, wherein the chromosome related abnormality is aneuploidy or polyploidy.

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33. (Original) The method of claim 31, wherein the method is used in preimplantation diagnosis or in prenatal screening.

Claim 34 (Canceled)

35. (Currently Amended) A set of PNA probes of 10 to 30 subunits in length for the detection, identification or enumeration of human chromosomes X, Y, 18 and 13/21 as a pair wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$, where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

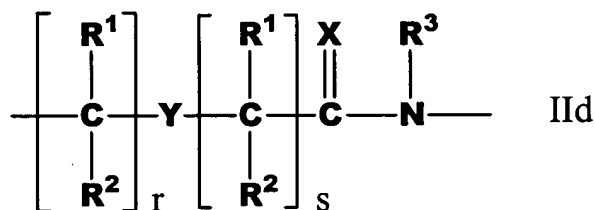
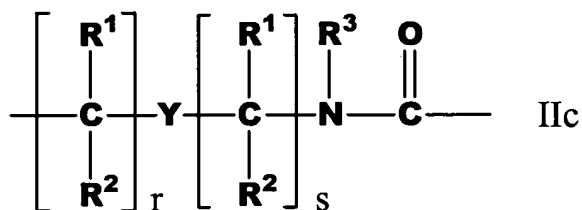
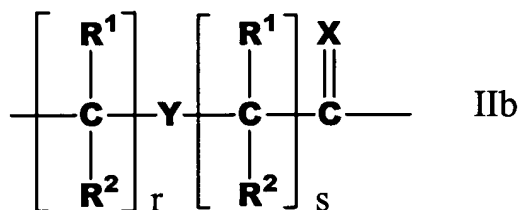
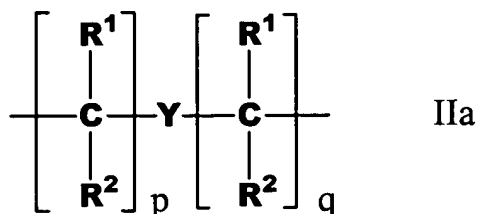
each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

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each of A^1-A^n and B^1-B^n are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R^3N^+ ; or

(b) A is a group of formula (IIId) and B is CH;



where:

X is O, S, Se, NR^3 , CH_2 or $C(CH_3)_2$;

Y is a single bond, O, S or NR^4 ;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R^1 and R^2 is independently selected from the group consisting of hydrogen, (C_1-C_4) alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

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each R^3 and R^4 is independently selected from the group consisting of hydrogen, (C_1-C_4) alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C_1-C_4) alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is $-CO_2H$, $-CONR'R''$, $-SO_3H$ or $-SO_2NR'R''$ or an activated derivative of $-CO_2H$ or $-SO_3H$; and

I is $-NHR'''R''''$ or $-NR'''C(O)R''''$, where R' , R'' , R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:
the one or more PNA probes of the set specific for detecting human chromosome X comprise a probing nucleobase sequence selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9), or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome Y comprise a probing nucleobase sequence selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16), or the complement to any of the foregoing sequences;

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the one or more PNA probes of the set specific for detecting human chromosome 18 comprise a probing nucleobase sequence selected from the group consisting of:

TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118) or the complement to any of the foregoing sequences;

the one or more PNA probes of the set specific for detecting human chromosome 13/21 comprise a probing nucleobase sequence selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences.

36. (Currently Amended) A kit ~~suitable for performing an assay which detects the presence, absence or number of human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 or 20, as well as 13/21 as a pair, in a sample, wherein said kit comprises~~ comprising:

- a) one or more PNA probes of 10 to 30 subunits in length wherein at least one probe comprises a probing nucleobase sequence, ~~at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements,~~ selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-

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ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA
 (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-
 GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG
 (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-
 ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-
 GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC
 (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-
 GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq.
 ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-
 GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID
 No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-
 GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq.
 ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-
 TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-
 AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27);
 GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-
 AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID
 No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-
 ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID
 No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-
 GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq.
 ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-
 AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID
 No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-
 GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq.
 ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-
 CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID
 No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-
 CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID
 No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-
 TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID
 No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-

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AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT
 (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-
 TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC
 (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127);
 ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-
 AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID
 No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-
 ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID
 No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-
 TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID
 No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-
 TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID
 No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-
 GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No.
 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-
 TGT-TGC (Seq. ID No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130);
 GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-
 AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No.
 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-
 TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No.
 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-
 GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID
 No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-
 CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG
 (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-
 TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-
 AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-
 GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA
 (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-
 AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA (Seq.
 ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG (Seq. ID No. 146); TAA-AAA-
 GAA-AGG-TTC-ATC (Seq. ID No. 147); GCT-TGC-AGA-TAC-TAC-AGA (Seq.

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ID No. 148); TGA-AAG-CGC-TTA-AAA-CGT (Seq. ID No. 149); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116) ; GCA-CTT-ACC-GGC-

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CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 157); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 158); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 159); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158); AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159), or the complement to any of the foregoing sequences; and

b) other reagents or compositions necessary to perform the assay.

37. (Currently Amended) The kit of claim 36, wherein ~~at~~ the probe or probes are unlabeled.

38. (Original) The kit of claim 37, wherein hybridization of the probing nucleobase sequence of the probe to the chromosome is detected using an antibody or antibody fragment, wherein the antibody or antibody fragment specifically binds, under antibody binding conditions, to the PNA/nucleic acid complex which forms under suitable hybridization conditions.

39. (Original) The kit of claim 38, comprising an antibody labeled with a detectable moiety.

40. (Original) The kit of claim 39, wherein the detectable moiety is selected from the group consisting of a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.

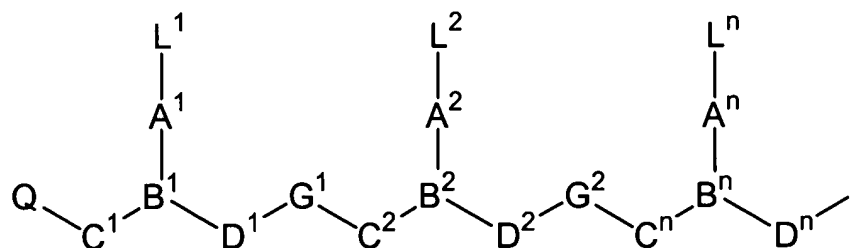
41. (Currently Amended) The kit of claim 36, wherein at least one ~~non-nucleic acid~~ PNA probe is labeled with a detectable moiety.

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42. (Original) The kit of claim 41, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.
43. (Original) The kit of claim 36, wherein analysis of *in-situ* hybridized specimens is performed using a microscope and camera, a flow cytometer or a slide based analysis system.

Claim 44 (Canceled)

45. (Currently Amended) A prenatal kit for the multiplex analysis of human chromosomes X, Y, 13, 18 and 21, wherein the kit comprises independently detectable PNA probes of 10 to 30 subunits in length for the individual detection of human chromosomes X, Y, 18, as well as human chromosomes 13 and 21 as a pair, and other reagents or components suitable to perform an assay wherein said PNA ~~probe or~~ probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, $(C_2-$

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C_6)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

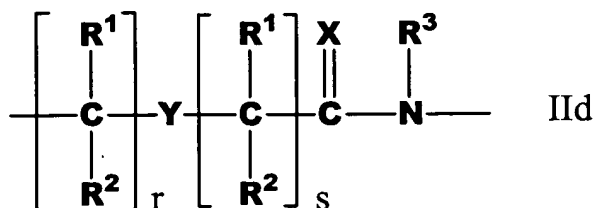
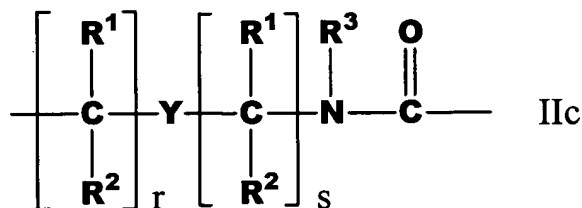
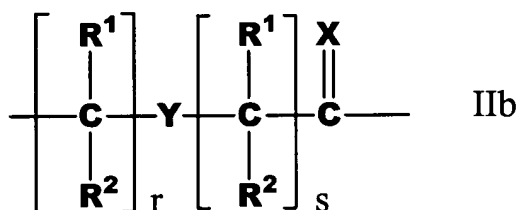
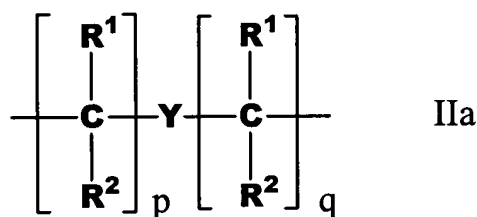
each of D^1-D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;

each of G^1-G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1-A^n and B^1-B^n are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IIId) and B is CH;



where:

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X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids; and wherein:

the PNA probes comprise a probing nucleobase sequence-selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17);

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CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No.

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51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-
TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID
No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-
TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA
(Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-
ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-
ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61);
CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-
ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No.
64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-
TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq.
ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-
CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-
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AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-
TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No.
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CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-
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ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No.
66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-
GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq.
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AAA-AAG-GTA-ATA (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG
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TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-
GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No.
74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-
AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID
No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-
ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID

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No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-

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CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158); and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159) or the complement to any of the foregoing sequences.